

20 40 60
 MGMSKSHSFFGYPLSIFIV VNEFCERFSYYGMRAILILY FTNFISWDDNLSTAIYHTFV
 80 100 120
 ALCYLTPILGALIADSWLGK FKTIVSLSIVYTIGQAVTSV SSINDLTDHNDGTPDSLPLV
 140 160 180
 HVVLSLIGLALIALGTGGIK PCVSAFGGDQFEEGQEKQRN RFFSIFYLAINAGSLLSTII
 200 220 240
 TPMLRVQQCGIHSKQACYPL AFGVPAALMAVALIVFVLGS GMYKKFKPQGNIMGKVAKCI
 260 280 300
 GFAIKNRFRHRSKAFPKREH WLDWAKEKYDERLISQIKMV TRVMFLYIPLPMFWALFDQQ
 320 340 360
 GSRWTLQATTMSGKIGALEI QPDQMOTVNAILIVIMVPIF DAVLYPLIAKCGFNFTSLKK
 380 400 420
 MAVGMVLASMAFVVAIVQV EIDKTLPVEFPKGNEVQIKVL NIGNNTMNISLPGEMVTLGP
 440 460 480
 MSQTNAFMFTFDVNLTRINI SSPGSPVTAVTDDFKQGQRH TLLVWAPNHYQVVKDGLNOK
 500 520 540
 PEKGENGIRFVNTFNELITI TMSGKVYANISSYNASTYQF FPSGIKGFTISSTEIPPQCQ
 560 580 600
 PNFNTFYLEFGSAYTYIVQR KNDSCEVKVFEDISANTVN MALQIPQYFLLTCGEVVFSV
 620 640 660
 TGLEFSYSQAPSNMKSVLQA GWLLTVAVGNIIVLIVAGAG QFSKQWAEYILFAALLLVVC
 680 700 708
 VIFAIMARFYTYINPAEIEA QFDEDEKKNRLEKSNPYFMS GANSQKQM

Fig. 1

[illegible]

Fig. 2A

1261 ggactcttcc taatccaaac ctatgctgga atgttacagt tagctaaaca gtccttgaag
 G L F L I Q T Y A G M L Q L A K Q S L K
 1321 aagcaagata ctccctcagta caacttaacg atagaggtgt ctgacaaaga tttcaagacc
 K Q D T P Q Y N L T I E V S D K D F K T
 1381 ctttggtttg tgcaaataca cggttattgat atcaatgatc agatcccat ctttgaaaaa
 L C F V Q I N V I D I N D Q I P I F E K
 1441 tcagattatg gaaacctgac tcttgctgaa gacacaaaca ttgggtccac catcttaacc
 S D Y G N L T L A E D T N I G S T I L T
 1501 atccaggcca ctgatgctga tgagccattt actgggagtt ctaaaattct gtatcatatc
 I Q A T D A D E P F T G S S K I L Y H I
 1561 ataaaggag acagtgagg acgcctggg gttgacacag atccccatac caacaccgga
 I K G D S E G R L G V D T D P H T N T G
 1621 tatgtcataa ttaaaaagcc tcttgatttt gaaacagcag ctggttccaa cattgtgttc
 Y V I I K K P L D F E T A A V S N I V F
 1681 aaagcagaaa atcctgagcc tctagtgttt ggtgtgaagt acaatgcaag ttcttttgcc
 K A E N P E P L V F G V K Y N A S S F A
 1741 aagttcacgc ttattgtgac agatgtgaat gaagcacctc aattttccca acacgtattc
 K F T L I V T D V N E A P Q F S Q H V F
 1801 caagcgaaag tcagtgagga tgtagctata ggcaactaaag tgggcaatgt gactgccaaag
 Q A K V S E D V A I G T K V G N V T A K
 1861 gatccagaag gtctggacat aagctattca ctgaggggag acacaagagg ttggcttaaa
 D P E G L D I S Y S L R G D T R G W L K
 1921 attgaccacg tgactggtga gatctttagt gtggtccat tggacagaga agccggaagt
 I D H V T G E I F S V A P L D R E A G S
 1981 ccatatcggg tacaagtggg ggccacagaa gtaggggggt cttccttaag ctctgtgtca
 P Y R V Q V V A T E V G G S S L S S V S
 2041 gagttccacc tgatccttat ggatgtgaat gacaaccctc ccaggctagc caaggactac
 E F H L I L M D V N D N P P R L A K D Y
 2101 acgggcttgt tcttctgcca tcccctcagt gcacctggaa gtctcatttt cgaggctact
 T G L F F C H P L S A P G S L I F E A T
 2161 gatgatgatc agcacttatt tcgggggtccc cattttacat tttccctcgg cagtgggaagc
 D D D Q H L F R G P H F T F S L G S G S
 2221 ttacaaaacg actgggaagt ttccaaaatc aatgggtactc atgcccgact gtctaccagg
 L Q N D W E V S K I N G T H A R L S T R
 2281 cacacagact ttgaggagag ggcgtatgtc gtcttgatcc gcatcaatga tgggggtcgg
 H T D F E E R A Y V V L I R I N D G G R
 2341 ccacccttgg aaggcattgt ttctttacca gttacattct gcagttgtgt ggaaggaagt
 P P L E G I V S L P V T F C S C V E G S
 2401 tgtttccggc cagcaggtca ccagactggg ataccactg tgggcatggc agttggtata
 C F R P A G H Q T G I P T V G M A V G I

Fig. 2B

2461	ctgctgacca L L T	cccttctggt T L L	gattgggtata V I G I	atttttagcag I L A	ttgtgttttat V V F	ccgcataaag I R I K
2521	aaggataaag K D K	gcaaagataa G K D	tgttgaaagt N V E S	gctcaagcat A Q A	ctgaagtcaa S E V	acctctgaga K P L R
2581	agctgaattt S	gaaaagggaat	gtttgaattt	atatagcaag	tgctattttca	gcaacaacca
2641	tctcatccta	ttactttttca	tctaacgtgc	attataattt	tttaaacaga	tattccctct
2701	tgtccttttaa	tatttgctaa	atatttcttt	tttgaggtgg	agtcttgctc	tgtcgcccag
2761	gctggagtac	agtgggtgta	tcccagctca	ctgcaacctc	cgctcctcgg	gttcacatga
2821	ttctcctgcc	tcagcttcct	aagtagctgg	gtttacaggc	acccaccacc	atgcccgact
2881	aattttttgta	tttttaataag	agacgggggt	tcgccatttg	gccaggctgg	tcttgaactc
2941	ctgacgtcaa	gtgatctgcc	tgcttgggtc	tcccaataca	ggcatgaacc	actgcaccca
3001	cctactttaga	tattttcatgt	gctatagaca	ttagagagat	ttttcatttt	tccatgacat
3061	ttttcctctc	tgcaaattgcc	ttagctactt	gtgtttttcc	cttttggggc	aagacagact
3121	cattaaatat	tctgtacatt	ttttctttat	caaggagata	tatcagtgtt	gtctcataga
3181	actgcctgga	ttccattttat	gtttttttctg	attccatcct	gtgtcccctt	catccttgac
3241	tcctttggta	tttcaactgaa	tttcaaacat	ttgtcagaga	agaaaaaagt	gaggactcag
3301	gaaaaataaaa	taaataaaaag	aacagccttt	tgcggccgcg	aattc	

Fig. 2C

20 40 60
 MARKKFSGLEISLIVLFVIV TIIAIALIVVLATKTPAVDE ISDSTSTPATTRVTTNPSSDS
 80 100 120
 GKCPNVLNDPVNVRINCIPE QFPTEGICAQRGCCWRPWND SLIPWCFFVDNHGYNVQDMT
 140 160 180
 TTSIGVEAKLNRIPSPTLFG NDINSVLFTTQNTPNRFRF KITDPNNRRYEVPHQYVKEF
 200 220 240
 TGPTVSDTLVDVKAQNPFS IQVIRKSNGKTLFDTSIGPL VYSDQYLQISARLPSDYIYG
 260 280 300
 IGEQVHKRFRHDLWSKWPFI FTRDQLPGDNNNNLYGHQTF FMCIEDTSGKSFGVFLMNSN
 320 340 360
 AMEIFIQPTPIVITYRVTGGI LDFYILLGDTPEQVVQQYQQ LVGLPAMPAYWNLGFQLSRW
 380 400 420
 NYKSLDVVKEVVRNRREAGI PFDTQVTDIDYMEDKKDFTY DQVAFNGLPQFVQDLHDHGQ
 440 460 480
 KYVIILDPAISIGRRANGTT YATYERGNTQHVWINESDGS TPIIGEVWPGLTVYPDFTNP
 500 520 540
 NCIDWWANECSEIFHQEVQYD GLWIDMNEVSSFIQGSTKGC NVNKLNYPPFTPDILDKLMY
 560 580 600
 SKTICMDAVQNWGKQYDVHS LYGYSMIAIEQAVQKVFPN KRSFILTRSTFAGSGRHAHAH
 620 640 660
 WLGDNTASWEQMEWSITGML EFSLFGIPLVGADICGFVAE TTEELCRRWMQLGAFYPFSR
 680 700 720
 NHNSDGYEHQDPAFFGQNSL LVKSSRQYLTIQYTLPLFLY TLFYKAHVGETVARPVLHE
 740 760 780
 FYEDTNSWIEDTEFLWGPAL LITPVLKQGADTVSAYIPDA IWYDYESGAKRPWRKQVRDM
 800 820 840
 YLPADKIGLHLRGGYIPIQ EPDVTTTASRKNPLGLIVAL GENNTAKGDFFWDDGETKDT
 860 880 900
 IQNGNYILYTFVSNNLTLDI VCTHSSYQEGTTLAFQTVKI LGLTDSVTEVRVAENNQPMN
 920 940 960
 AHSNFTYDASNQVLLIADLK LNLGRNFSVQWNQIFSENER FNCYPDADLATEQKCTQRC
 980 1000 1020
 VVRTGSSLSKAPECYFPRQD NSYSVNSARYSSMGITADLQ LNTANARIKLPSDPISLTV
 1040 1060 1080
 EVKYHKNDMLQFKIYDPQKK RYEVVPLNIPTTPISTYED RLYDVEIKENPFGIQIRRS
 1100 1120 1140
 SGRVIWDSWLPGFANDQFI QISTRLPSEYIYGFGVEHT AFKRDLNWNTWGMFTRDQPP
 1160 1180 1200
 GYKLNSYGFHPYMALEEEG NAHGVFLLSNAMDVTFQPT PALTYRTVGGILDFYMFLLGP
 1220 1240 1260
 TPQVATKQYHEVIGHVMPA YWALGFQLCRYGYANTSEVR ELYDAMVAANIPYDVQYTDI

Fig. 3A

1280 1300 1320
DYMERQLDFTIGEAFQDLPO FVDKIRGEGMRYIIILDPAI SNETKTYPAFERGQQNDVF
1340 1360 1380
VKWPNTNDICWAKVWPDLPN ITIDKLTLEDEAVNASRAHV AFPDFFRTSTAEWWAREIVD
1400 1420 1440
FYNEKMKFDGLWIDMNEPSS FVNGTTTNQCRNDELNYPPY FPELTKRTDGLHFRTICMEA
1460 1480 1500
EQILSDGTSVLHYDVHNLGY WSQMKPTHDALQKTTGKRGV VISRSTYPTSGRWGGHWLGD
1520 1540 1560
NYARWDNMDKSIIGMMEFSL FGISYTGADICGFFNNSEYH LCTRWMQLGAFYPYSRHNHI
1580 1600 1620
ANTRRQDPASWNETFAEMSR NILNIRYTLPLPYFYTMHEI HANGGTVIRPLLHEFFDEKP
1640 1660 1680
TWDIFKQFLWGPAFMVTPVL EPYVQTVNAYVPNARWFDYH TGKDIGVRGQFQTFNASYDT
1700 1720 1740
INLHVRGGHILPCQEPAQNT FYSRQKHKMLIVAADDNQMA QGSLFWDDGESIDTYERDLY
1760 1780 1800
LSVQFNLNQTTLTSTILKRG YINKSETRLGSLHVWGKGT PVNAVTLTYNGNKNSLPFNE
1820 1827
DTTNMILRIDLTTHNVTLEE PIEINWS

Fig. 3B

[illegible]

Fig. 4A

1021 gagatgagat ccaagtaa at aagacccaaa tcccggacac ggtcacacaa tactcggagc
 R D E I Q V N K T Q I P D T V T Q Y S E
 1081 tgtaccatga cttcaccacc acgcaggtgg gaatgcacga cattgtccgc agcttccggc
 L Y H D F T T T Q V G M H D I V R S F R
 1141 agaccatgga ccaatacagc acggagcccg gcagatacag gttcatgggg actgaagcct
 Q T M D Q Y S T E P G R Y R F M G T E A
 1201 atgcagagag tattgacagg accgtgatgt actatggatt gccatttatc caagaagctg
 Y A E S I D R T V M Y Y G L P F I Q E A
 1261 attttccctt caacaattac ctcagcatgc tagacactgt ttctgggaac agcgtgtatg
 D F P F N N Y L S M L D T V S G N S V Y
 1321 aggttatcac atcctggatg gaaaacatgc cagaaggaaa atggcctaac tggatgattg
 E V I T S W M E N M P E G K W P N W M I
 1381 gtggaccaga cagttcacgg ctgacttcgc gtttggggaa tcagtatgtc aacgtgatga
 G G P D S S R L T S R L G N Q Y V N V M
 1441 acatgcttct ttacacactc cctggaactc ctataactta ctatggagaa gaaattggaa
 N M L L F T L P G T P I T Y Y G E E I G
 1501 tgggaaatat tgtagccgca aatctcaatg aaagctatga tattaatacc ctctgcgtcaa
 M G N I V A A N L N E S Y D I N T L R S
 1561 agtcaccaat gcagtgggac aatagttcaa atgctggttt ttctgaagct agtaaacacct
 K S P M Q W D N S S N A G F S E A S N T
 1621 ggttacctac caattcagat taccacactg tgaatgttga tgtccaaaag actcagccca
 W L P T N S D Y H T V N V D V Q K T Q P
 1681 gatcggtctt gaagttatat caagatttaa gtctacttca tgccaatgag ctactcctca
 R S A L K L Y Q D L S L L H A N E L L L
 1741 acaggggctg gttttgccat ttgaggaatg acagccacta tgttggtgtac acaagagagc
 N R G W F C H L R N D S H Y V V Y T R E
 1801 tggatggcat cgacagaatc tttatcgtgg ttctgaattt tggagaatca acactgttaa
 L D G I D R I F I V V L N F G E S T L L
 1861 atctacataa tatgatttcg ggccttcccg ctaaaataag aataaggtta agtaccatt
 N L H N M I S G L P A K I R I R L S T N
 1921 ctgccgacaa aggagtaaa gttgatacaa gtggcatttt tctggacaag ggagagggac
 S A D K G S K V D T S G I F L D K G E G
 1981 tcatctttga acacaacagc aagaatctcc ttcacgcca aacagctttc agagatagat
 L I F E H N T K N L L H R Q T A F R D R
 2041 gctttgtttc caatcgagca tgctattcca gtgtactgaa catactgtat acctcgtgtt
 C F V S N R A C Y S S V L N I L Y T S C
 2101 aggcaacctt atgaagagat gaagacactg gcatttcagt gggattgtaa gcatttgtaa
 2161 tagcttcatg tacagcatgc tgcttggtga acaatcatta attcttcgat atttctgtag
 2221 cttgaatgta accgctttaa gaaaggttct caaatgtttt gaaaaaata aaatgtttaa
 2281 aagt

Fig. 4B

Expression of Phage Inserts as GST Fusion

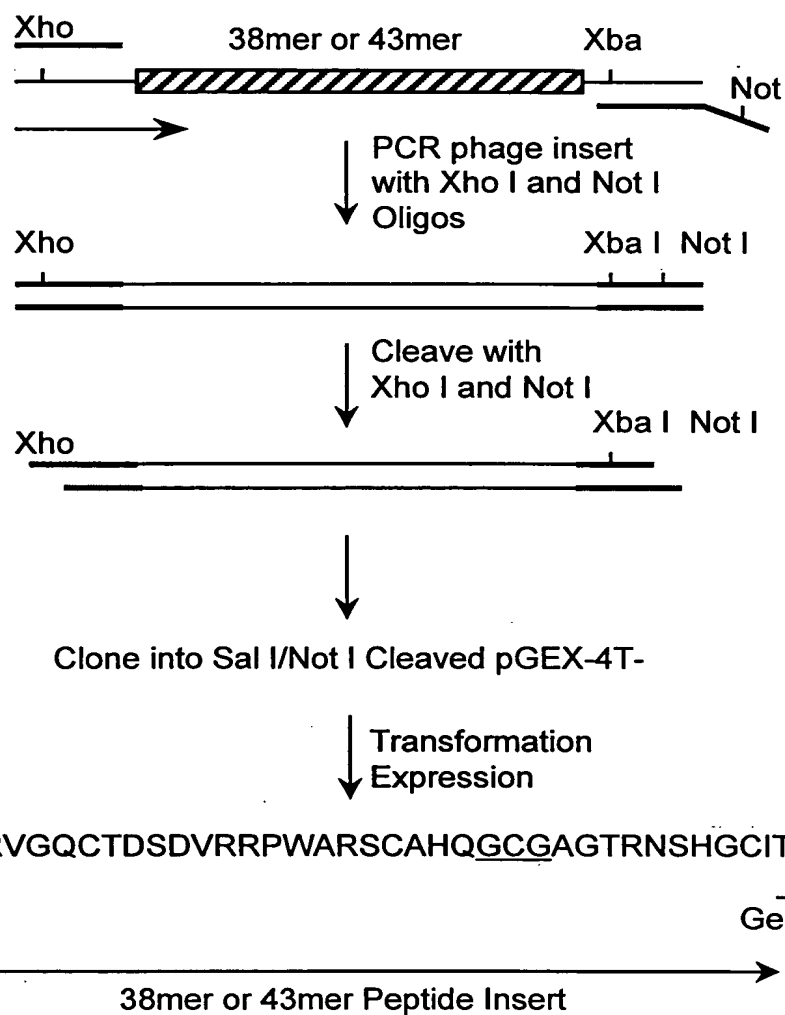


Fig. 5A

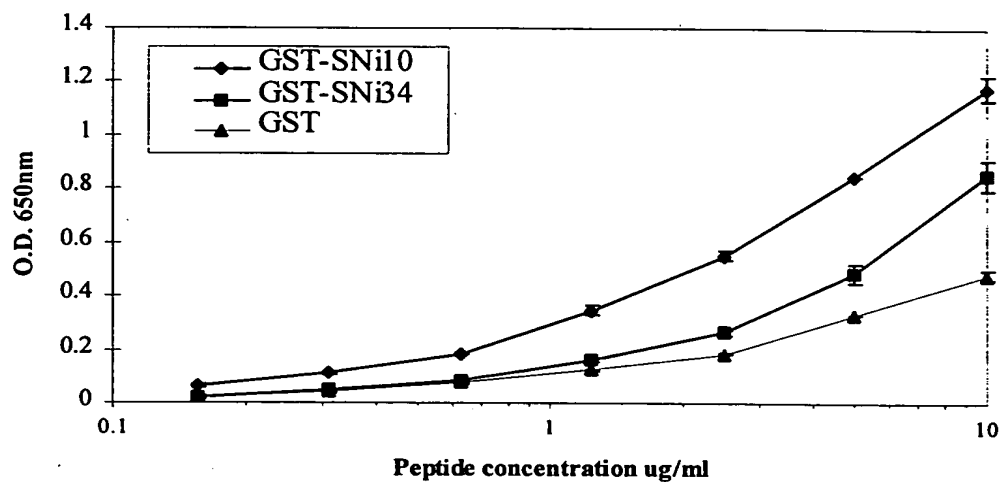
P31	1	10	20	30	Clone #
	SARDSGPAEDGSRAVRLNGVENANTRKSSRSNPRGRRHP				
	SARDSGPAEDGSRAVRLNG				101
		DGSRAVRLNGVENANTRKSSR			102
			ENANTRKSSRSNPRGRRHP		103
			TRKSSRSNPRG		119
Pax2	1	10	20	30	Clone #
	STPPSREAYSRPYSDSDSDTNAKHSSHNRRLRTRSRPN				
	STPPSREAYSRPYSDSDSD				104
		SRPYSDSDSDTNAKHSSHNR			105
			TNAKHSSHNRRLRTRSRPN		106
DCX8	1	10	20	30	Clone #
	RYKHDIGCDAGVDKKSSSVRGCGAHSSPPRAGRGRGTMTVSRL				
	RYKHDIGCDAGVDKKSSSVRGCG				107
		GCDAGVDKKSSSVRGCGAHSSPPRA			108
			GAHSSPPRAGRGRGTMTVSRL		109

Fig. 5B

P31	1	10	20	30	Clone #
	SARDSGPAEDGSRAVRLNGVENANTRKSSRSNPRGRRHP				
			ENANTRKSSRSNPRGRRHP		103
			ENANTRKSSR		110
			TRKSSRSNPRG		119
			RKSSRSNPRG		111
			SNPRGRRHP		112
Pax2	1	10	20	30	Clone #
	STPPSREAYSRPYSDSDSDTNAKHSSHNRLRLTRSRPN				
			TNAKHSSHNRLRLTRSRPN		106
			TNAKHSSHN		113
			SSHNRLRLTR		114
			RRLRLTRSRPN		115
SNi10	1	10	20	30	Clone #
	RVGQCTDSDVRRPWARSCAHQCGAGTRNSHGCITRPLRQASAH				
		RVGQCTDSDVRRPWARSCA			116
		VRRPWARSCAHQCGAGTRNS			117
			GTRNSHGCITRPLRQASAH		118

Fig. 5C

A



B

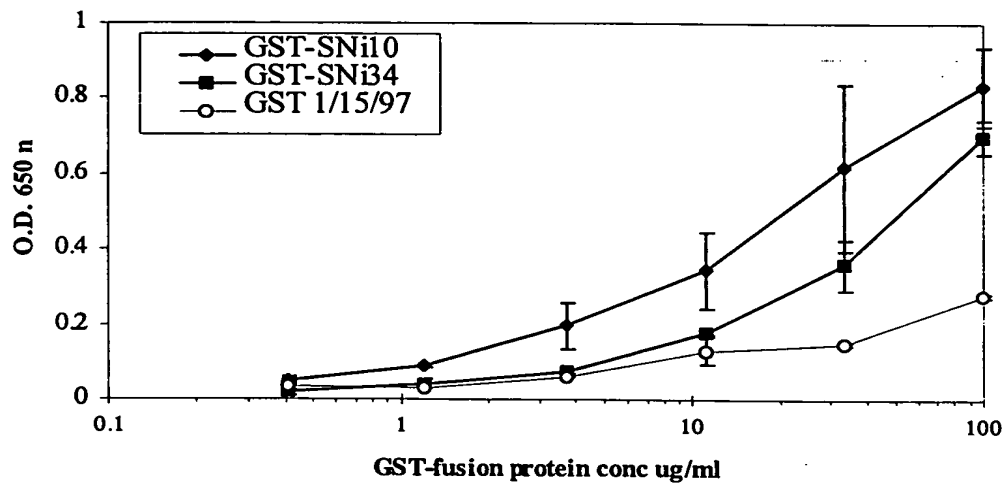


Fig. 6

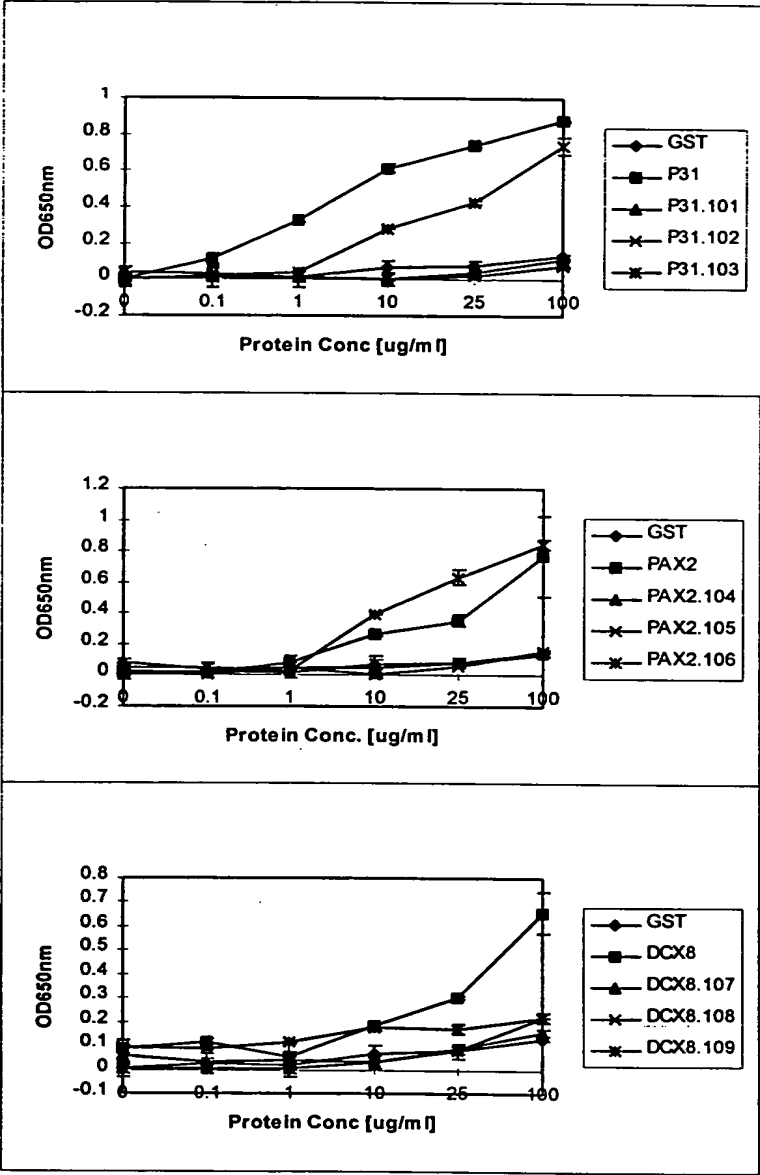
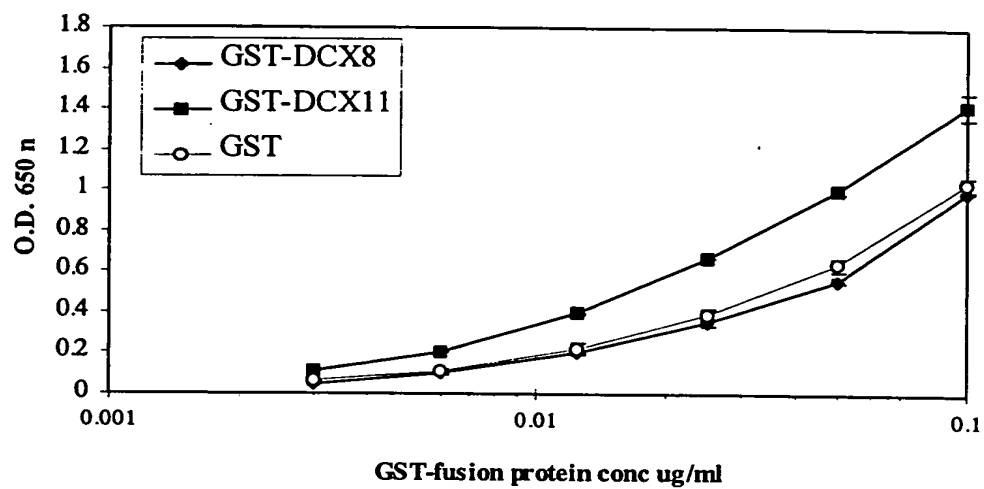
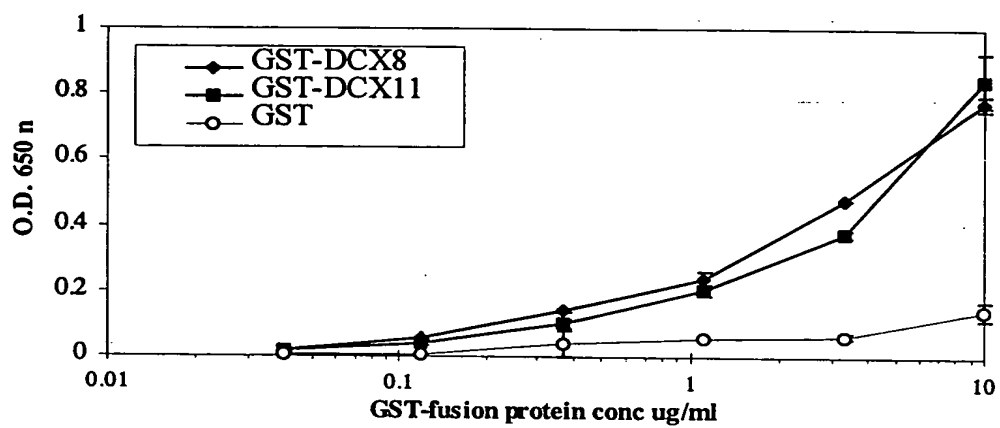
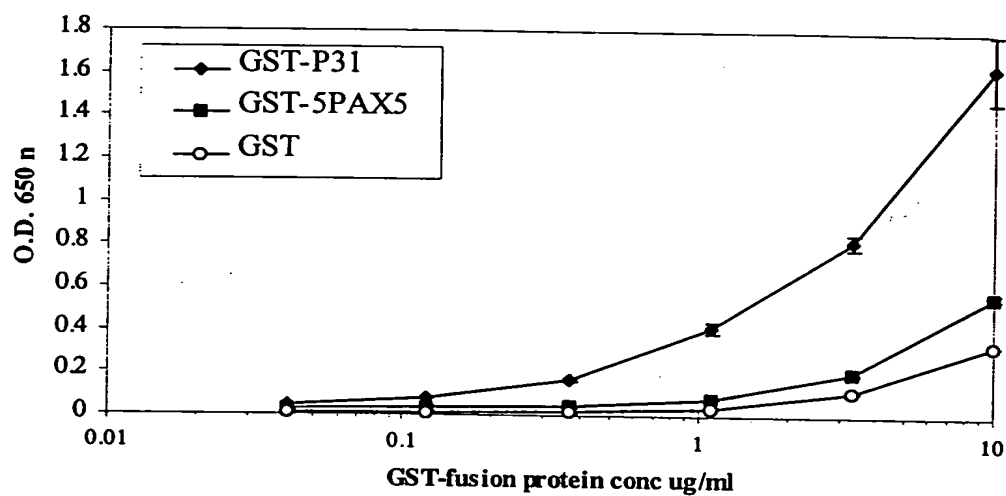


Fig. 7A-C

D**E****Fig. 7 D-E**

F



G

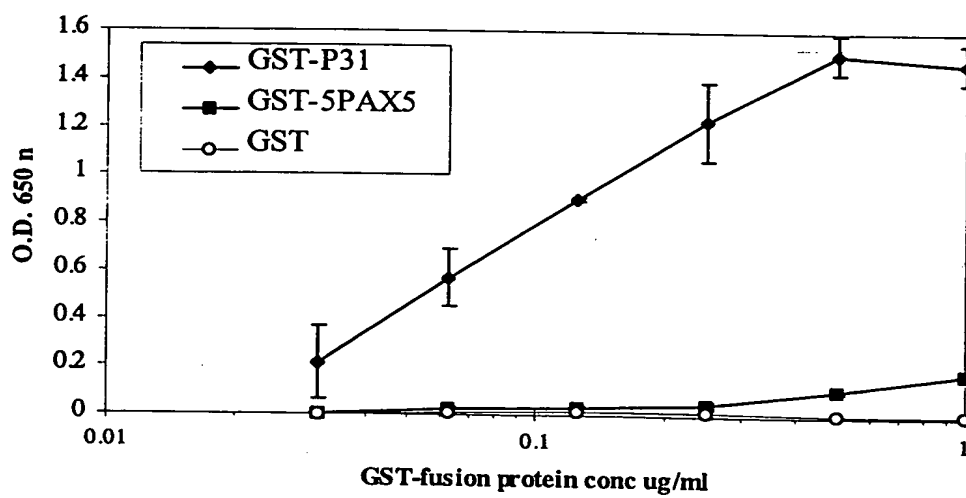
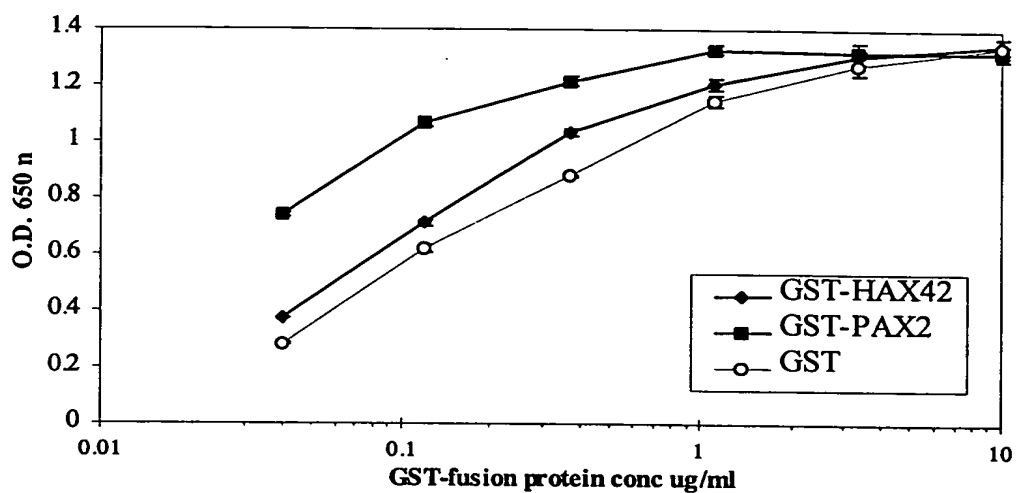


Fig. 7 F-G

H



I

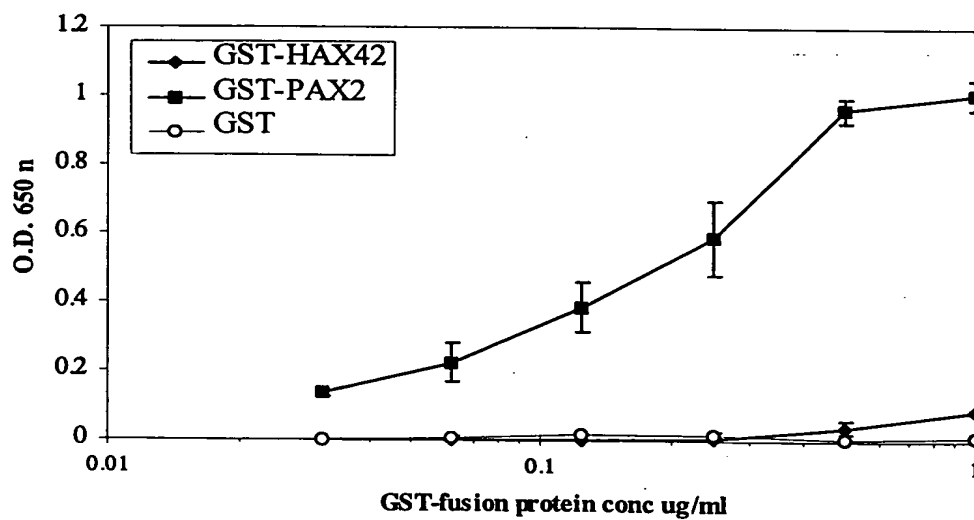
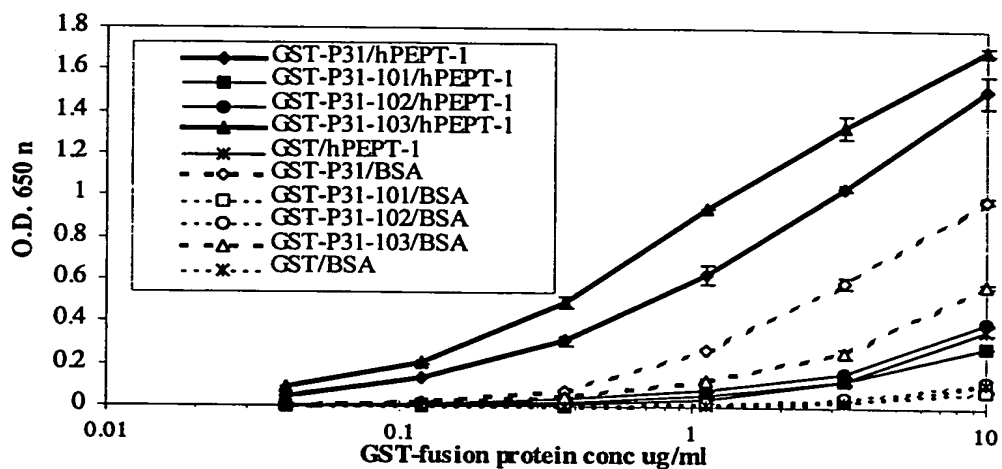


Fig. 7 H-I

J



K

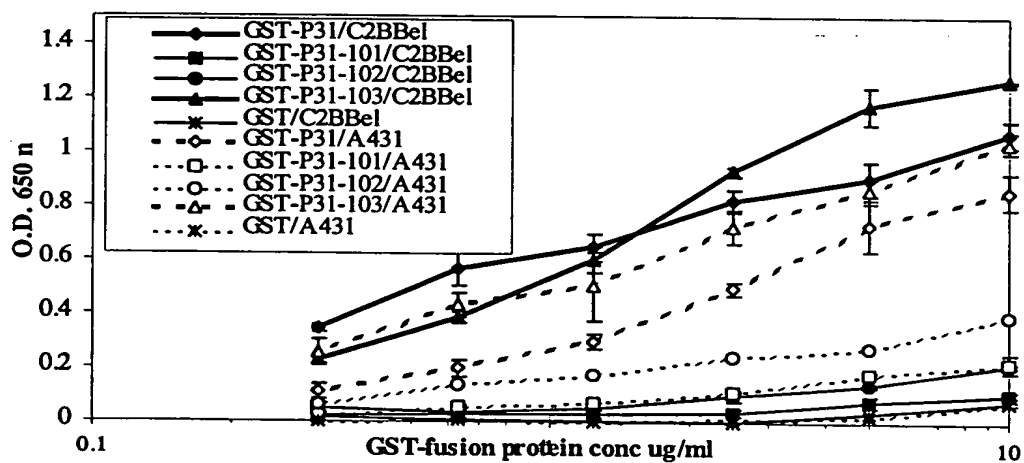
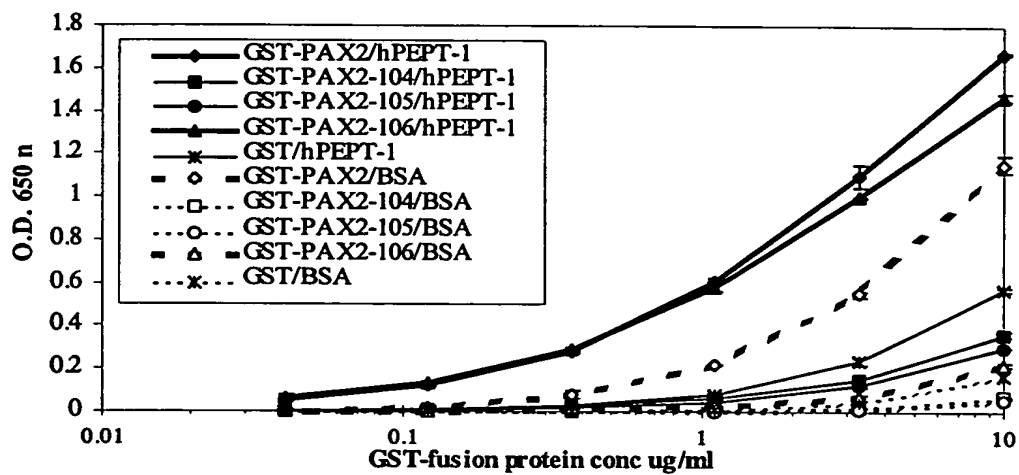


Fig. 7 J-K

L



M

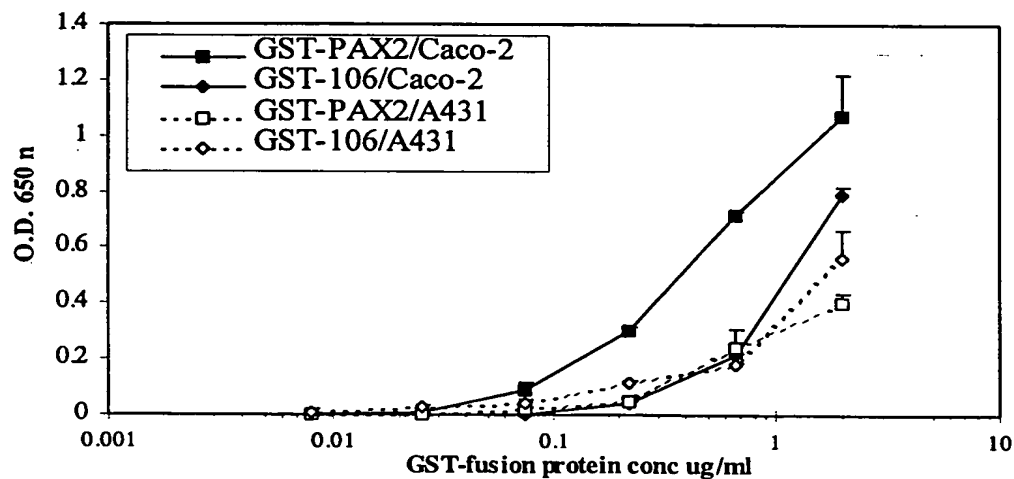
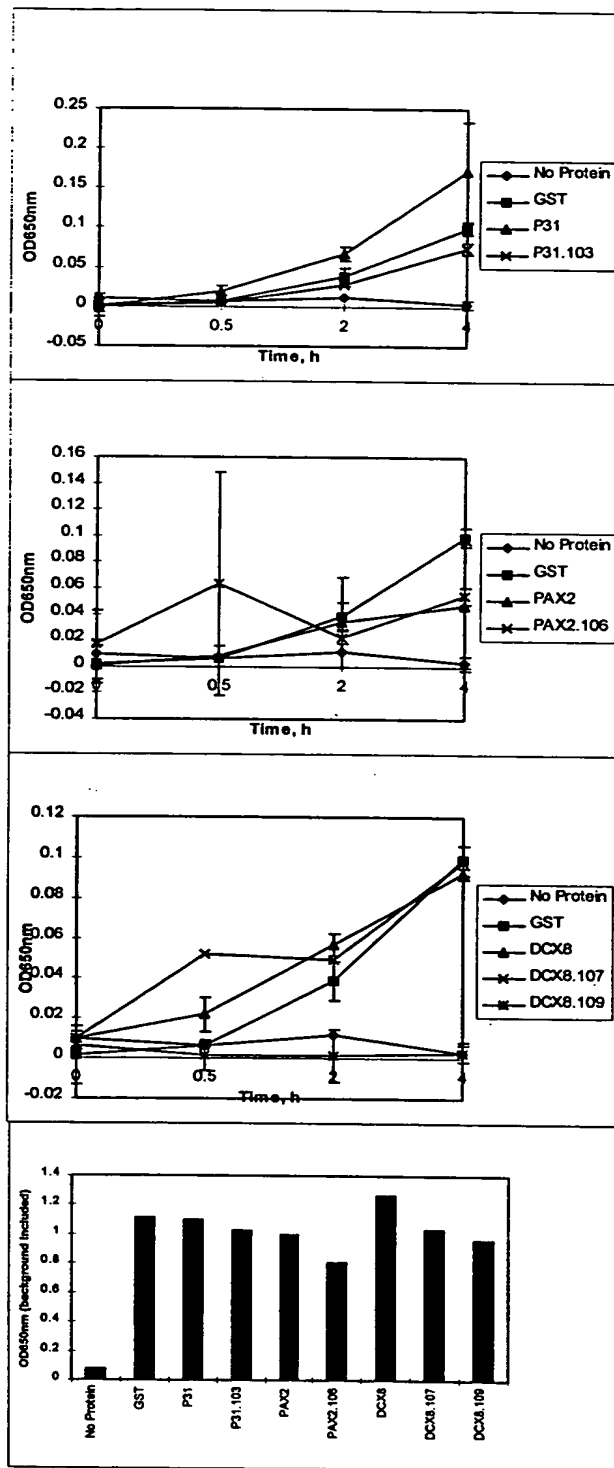
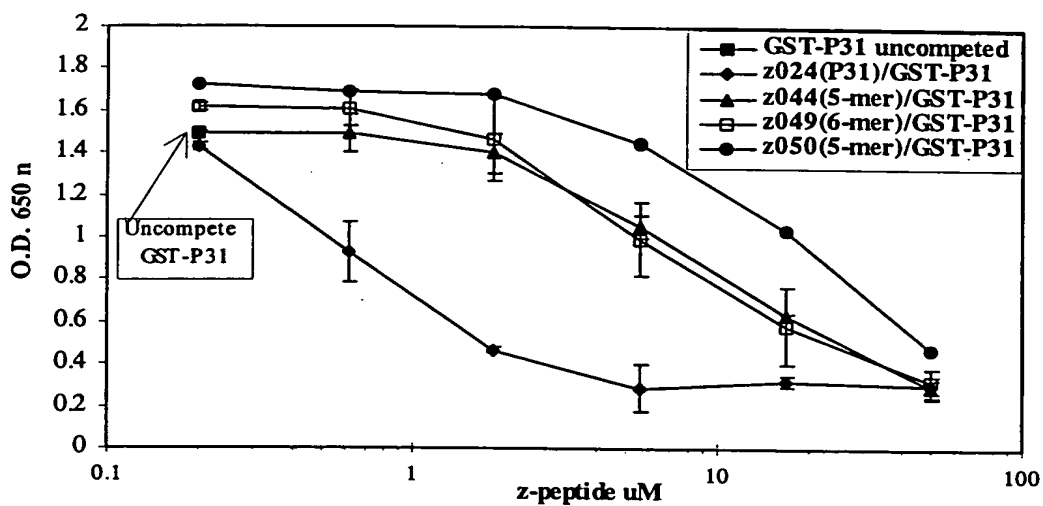


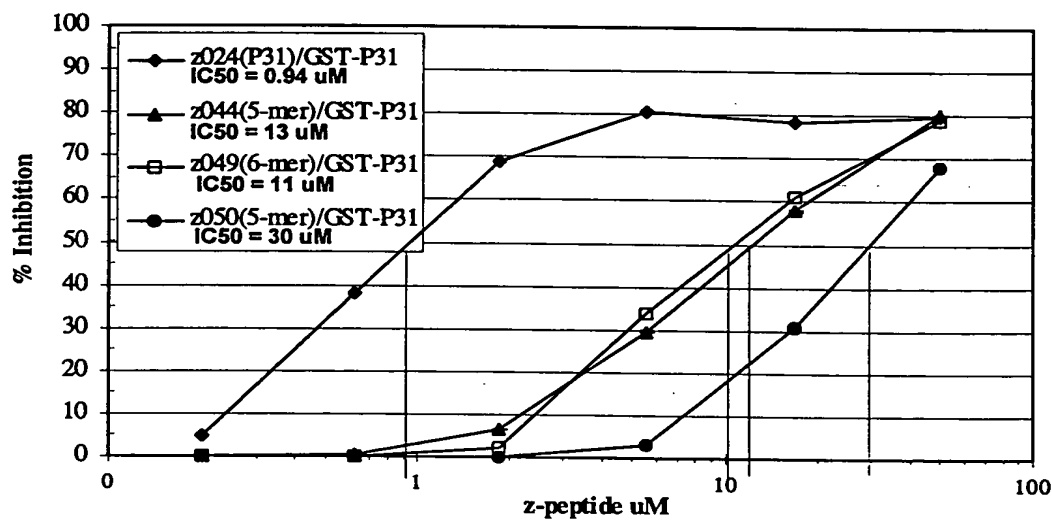
Fig. 7 L-M



Figs. 8 A-D



A



B

Fig. 9

P31

Peptide Name	Sequence	1	10	20	30	40	PI	IC ₅₀	GST/C2BBel
ELAN024 (P31)	SARDSGPAEDGSRVRLNGVENANTRKSSRSNPRGRHPG						11.88	0.5-2.2	+++
101	SARDSGPAEDGSRVRLNG								-
102	DGSRVRLNGVENANTRKSSR								++
103	ENANTRKSSRSNPRGRHP								-
110	ENANTRKSSR								-
111	RKSSRSNPRG								-
112	SNPRGRHP								-
119	TRKSSRSNPRG								
Z28	ZENANTRKSSRSNPRGRHPG						12.28	0.5-1.7	
Z29	ZTRKSSRSNPRG						12.40	5.5-15	
Z30	ZENANTRKSSRSNPRG						11.81	>50	
Z31	ZTRKSSRSNPRGRHPG						12.70	0.6-3.2	
Z39	ZENANTRKSSR						10.89	>50	
Z40	ZSNPRGRHPG						12.40	5.9-29	
Z41	ZENANT						3.75	>50	
Z42	ZANTRKS						11.05	>50	
Z43	ZTRKSS						11.05	>50	
Z44	ZRKSSR						12.11	13->50	
Z45	ZKSSRSN						11.05	40-48	
Z46	ZSSRSNPG						10.04	>50	
Z47	ZRSNPRG						12.40	>50	
Z48	ZSNPRG						10.04	>50	
Z49	ZPRGRH						12.40	11-20	
Z50	ZRRHPG						12.10	30	
Z51 (HepC core)	ZKSSRGN						12.40	>50	
Z52 (HepC P26664)	ZKTSERSQPRGRHPG						12.10	9.8	
Z53	ZTrKSSrSNPrGrHPG							1.6	
Z54	ZTRKSSrSNPRGrHPG							1.6	
Z21 (HAX42)	SDHALGTNLRSDNAKEPGDYNCCGNGNSTGRKVFRRRPSAIFT						11.27	1.7	

Fig. 10A

PAX2

Peptide Name	Sequence	1	10	20	30	40	pI	IC ₅₀	GST/C2BBe1
ELAN018 (PAX2)	STPPSREAYSRPYSVDSDSDTNAKHSSHNRLRTRSRPNG						10.88 0.6-0.9, 1	+++	
104	STPPSREAYSRPYSVDSDSD								-
105	SRPYSVDSDSDTNAKHSSHN								-
106	TNAKHSSHNRLRTRSRPN								++
113	TNAKHSSHN								-
114	SSHNRLRTR								+/-
115	RRLRTRSRPN								+/-
Z32	ZTNAKHSSHNRLRTRSRPN						12.7	1.2	
Z33	ZTNAKHSSHNRLRTR						12.58 1.6		
Z34	ZSSHNRRLRTRSRPN						12.7	1.6, 1.3, 0.68, 1.5	
Z35	ZSSHNRRLRTR						12.58 0.38 - 1.8, 2.7		
Z26	Z SEANLDGRKSRYSPPRNSSTRPTSPNSVHARYPSTDHD						10.88 7-8, 3		
Z38	Z SRANTDGRKSRYSPPRNSSTEPRLSPNSVHARYPSTDHD						10.88 1.7, 0.9		
Z55	ZTNAKHSSHN							42	
Z56	ZRRLRTRSRPN							1.7	
Z57	ZRRLRTRSR							1.9	
Z58	ZRRLRTR						3.4		
Z59	ZiLiTiSiPN							NOT DONE	
Z73	ZASHNRRLRTR						1.5, 5.5		
Z74	ZSAHNRRLRTR						6.2		
Z75	ZSSANRRRLRTR						1.6		
Z76	ZSSHARRLRTR						1.8		
Z77	ZSSHNAARLRTR						3.9, 5.2		
Z78	ZSSHNRALRTR						4.5, 4.6		
Z79	ZSSHNRARRTR						1.4		
Z80	ZSSHNRRLATR						3.4, 5.2		
Z81	ZSSHNRRLRAR						2.2		
Z82	ZSSHNRRLRTA						3.4		
Z21 (HAX42)	ZSDHALGTNLRSDNAKEPGDYNCCGNGNSTGRKVFNRFRPSAIP						11.27 0.7		

Fig. 10B

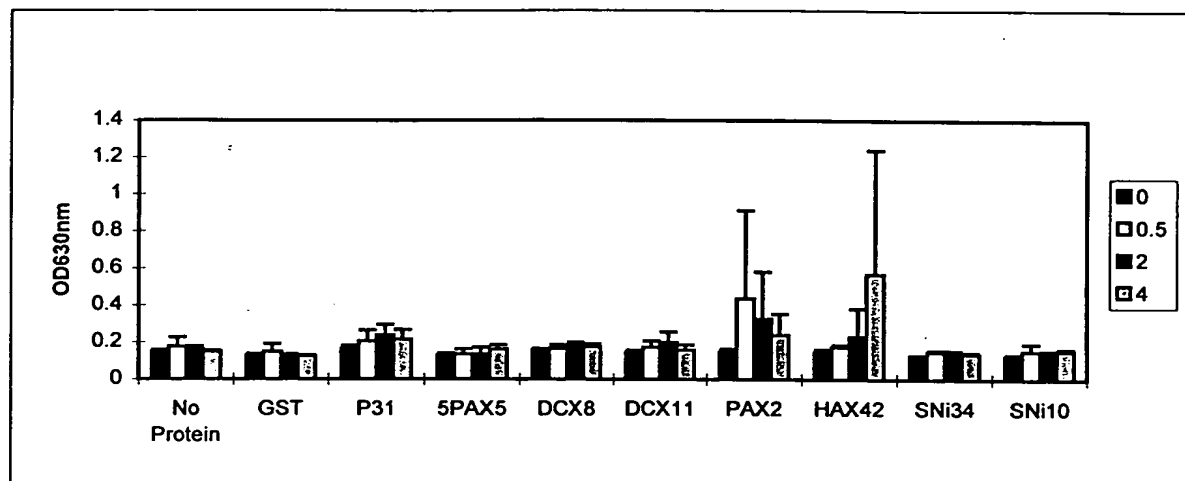
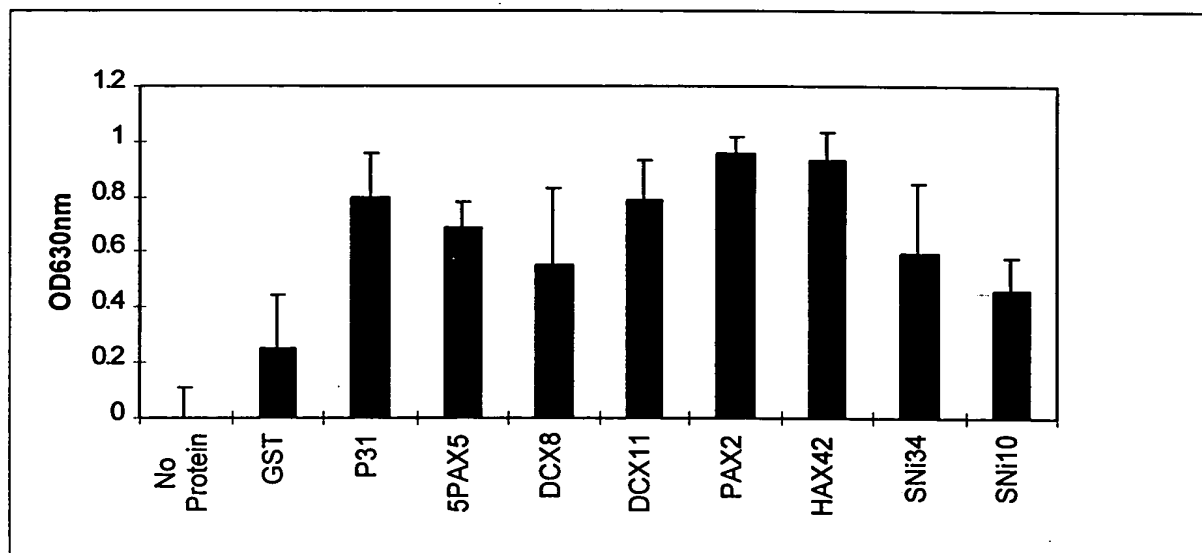
SNI10

Peptide Name	Sequence	PI	IC ₅₀	GST/C2BBel
ELAN016 (SNI10)	1 10 20 30 40 RVGQCTDSVRRPWARSCAHQCGAGTRNSHGCTIRPLRQASAH	10.19	0.22	++
116	RVGQCTDSVRRPWARSCA			-
117	VRRPWARSCAHQCGAGTRNS			+
118	GTRNSHGCTIRPLRQASAH			+/-
Z17	ZRVGQCTDSVRRPWARSCAH	8.66	3.6	
Z16C23	ZCGAGTRNSHGCTIRPLRQASAH	9.03	0.7	
Z36	ZVRRPWARSCAHQCGAGTRNS	11.62	0.27	
Z37	ZCTDSVRRPWARSC	8.01	3	

HAX42

Peptide Name	Sequence	PI	IC ₅₀	GST/C2BBel
ELAN021 (HAX42)	1 10 20 30 40 SDHALGTNLRSDNAKEPGDYNCCGNGNSTGRKVFNRRRPSAIP	11.27	5.5	++
ELAN018 (PAX2)	STPPSREAYSRPYSVDSDTNAKHSSHNRLRTRSRPNG	10.88	0.23	+++
Z26	ZSEANLDGRKSRYSPPRRNSSTRPRTSPNSVHARYPSTDHD	10.88	<0.2	
Z38	ZSRANTDGRKSRYSPPRRNSSTEPRLSVHARYPSTDHD	10.88	<0.2	
Z34 (PAX2 14mer)	ZSSHNRRLRTRSRPN	12.7	0.33	

Fig. 10C

**A****B****Fig. 11**

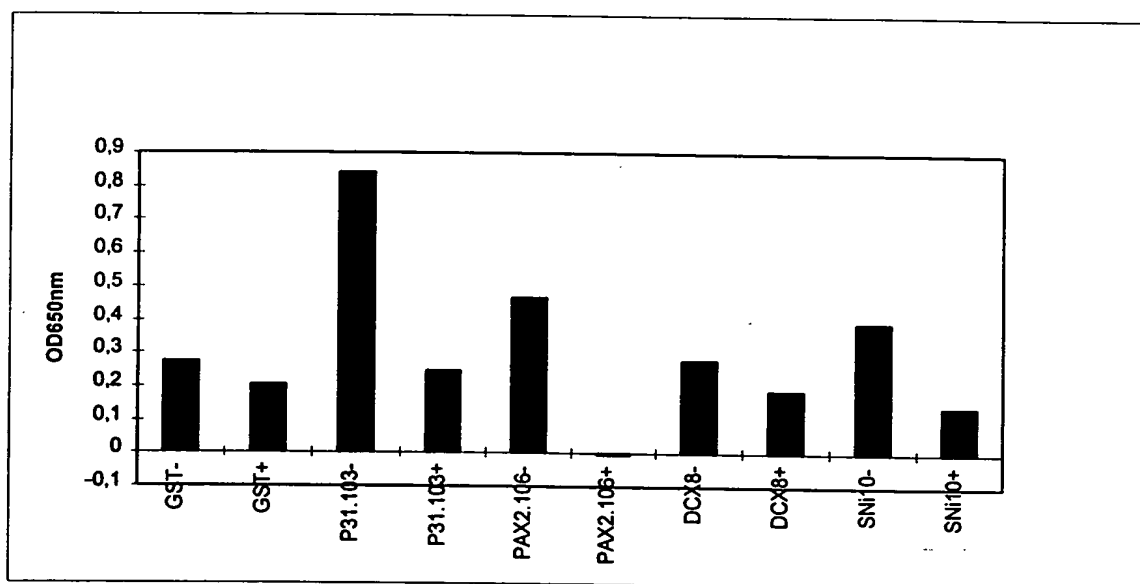
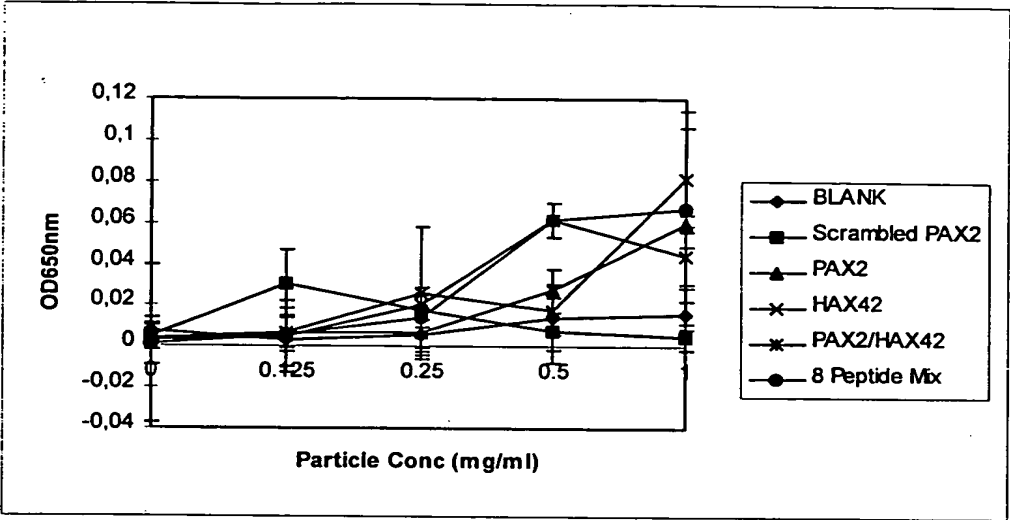
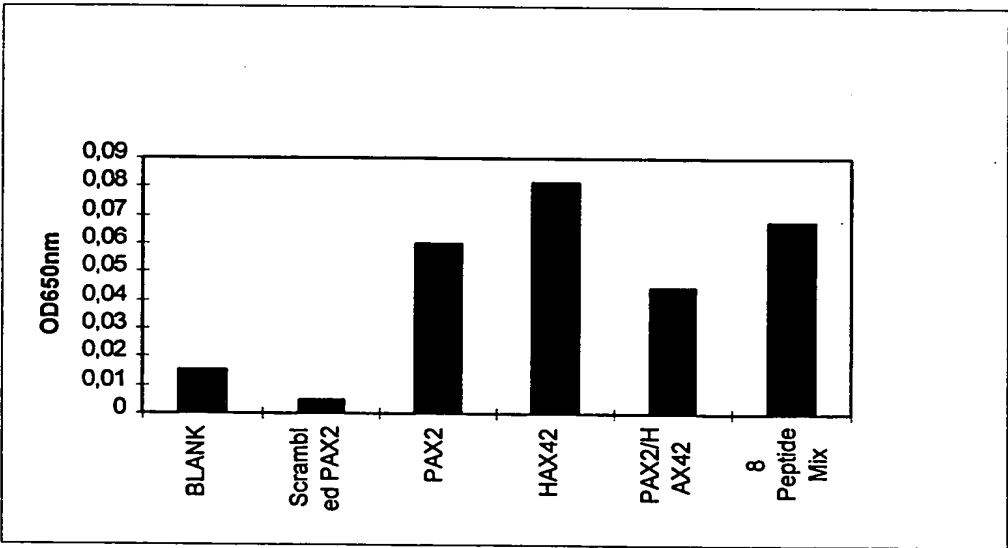


Fig. 12

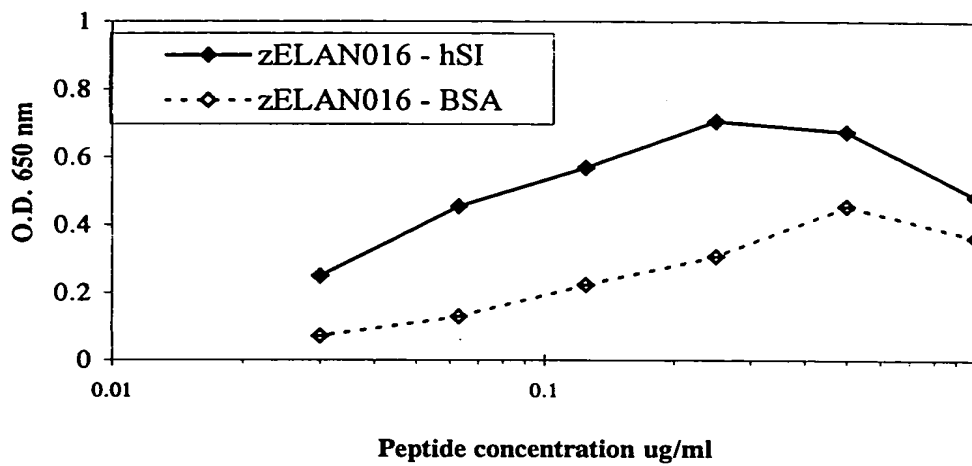
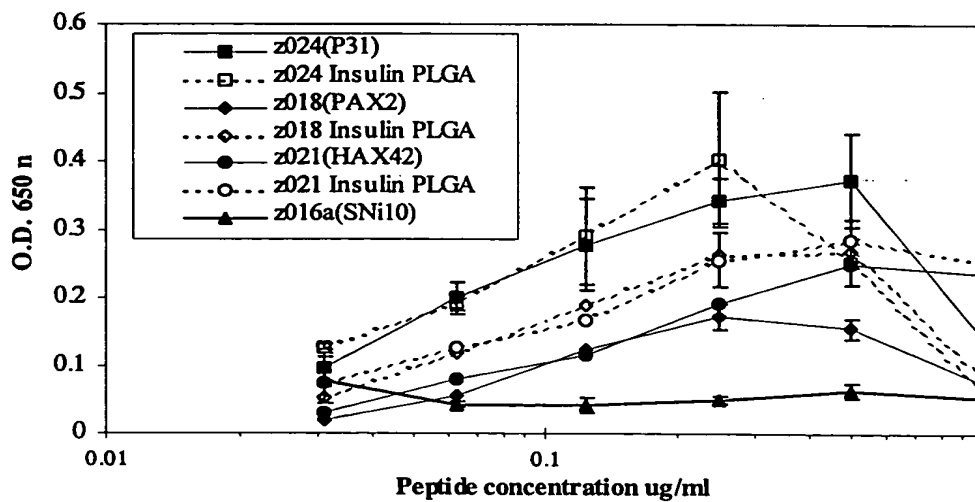


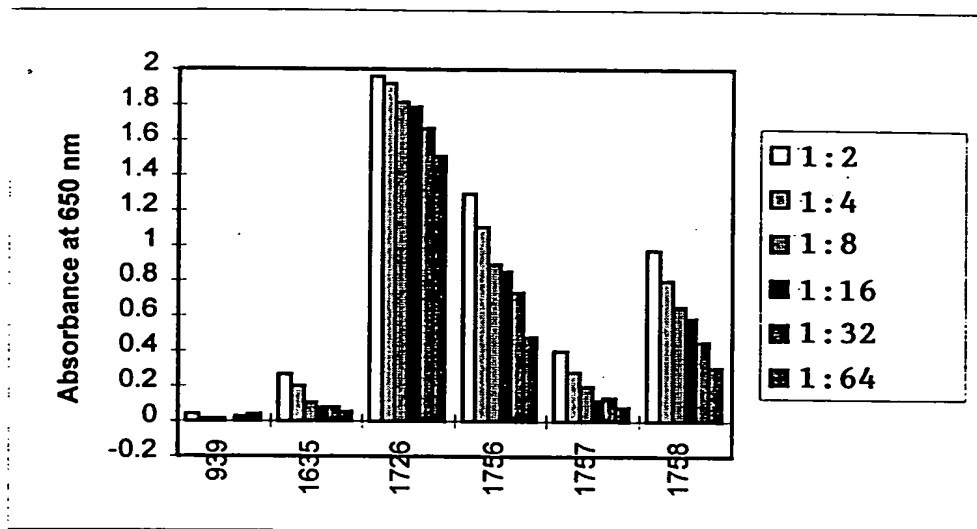
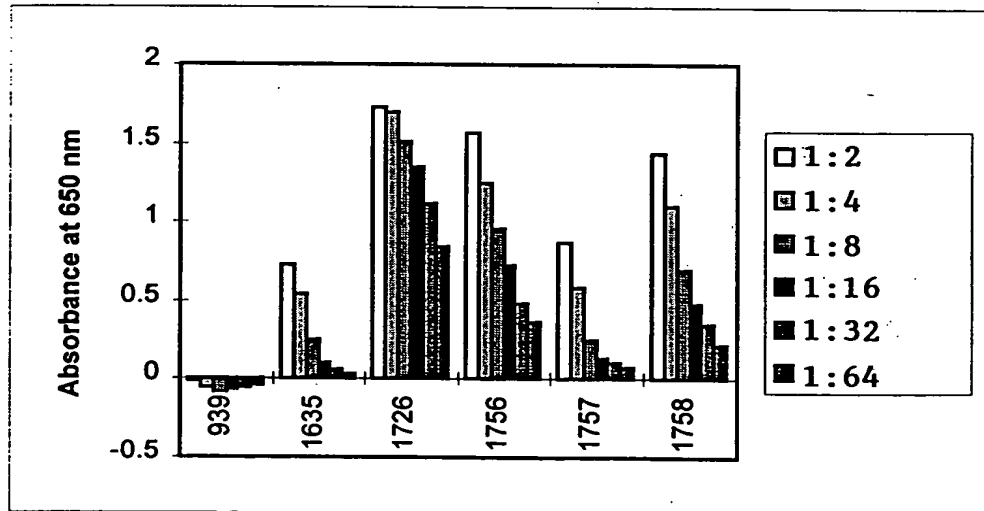
A

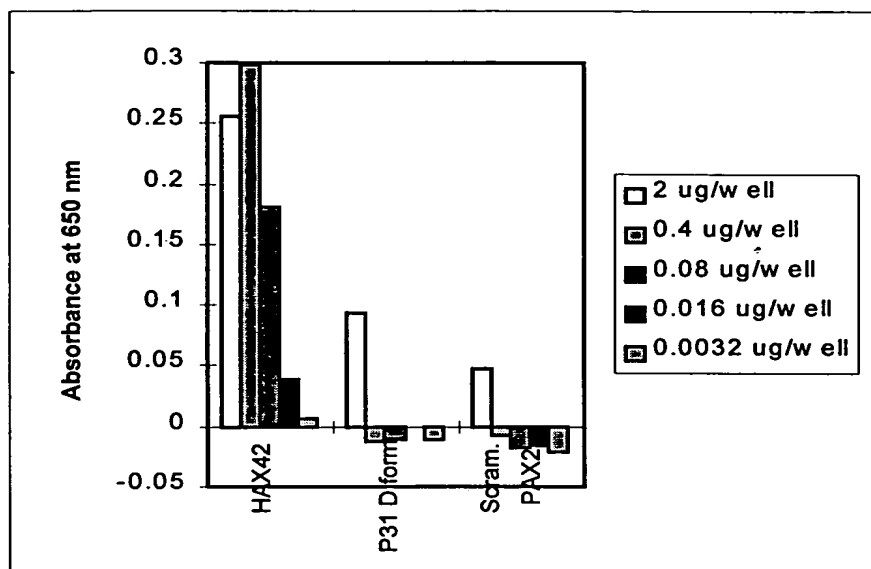


B

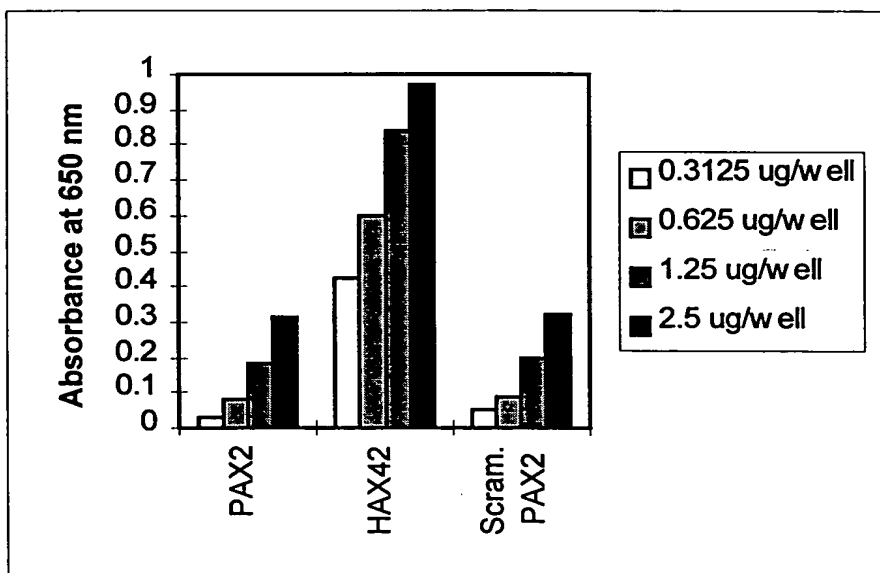
Fig. 13

A**B****Fig. 14**

**A****B****Fig. 15**

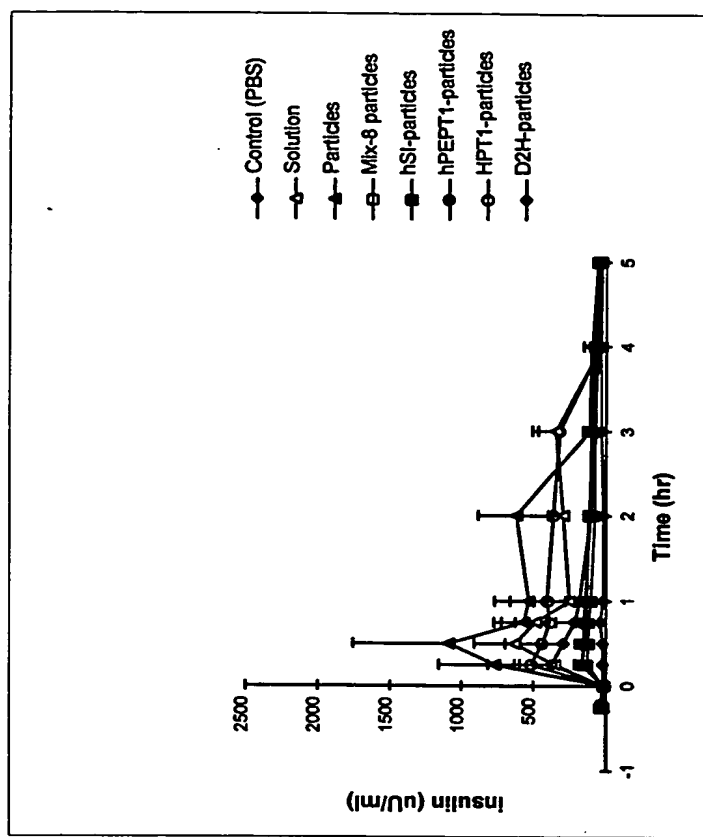


A

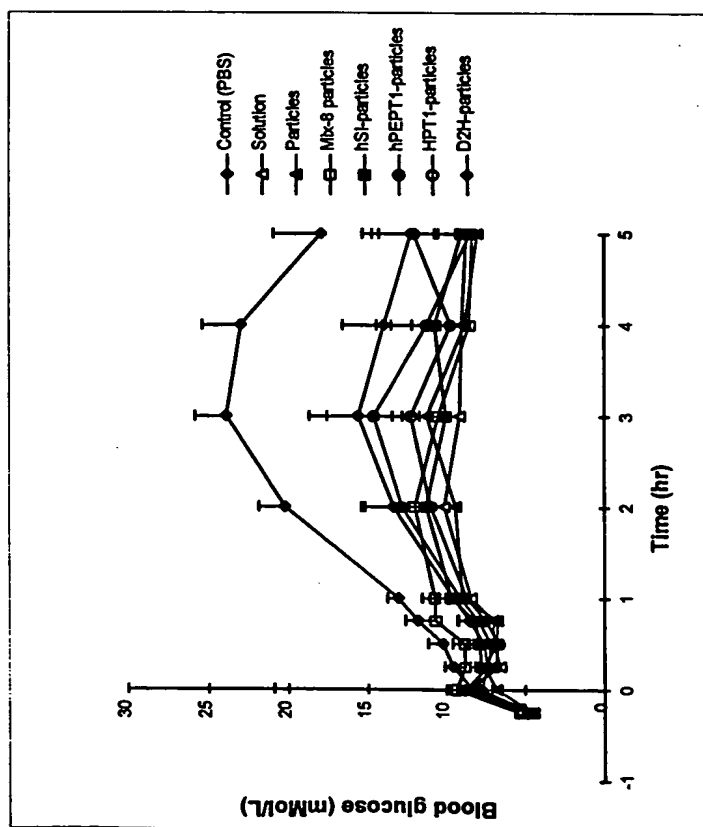


B

Fig. 16

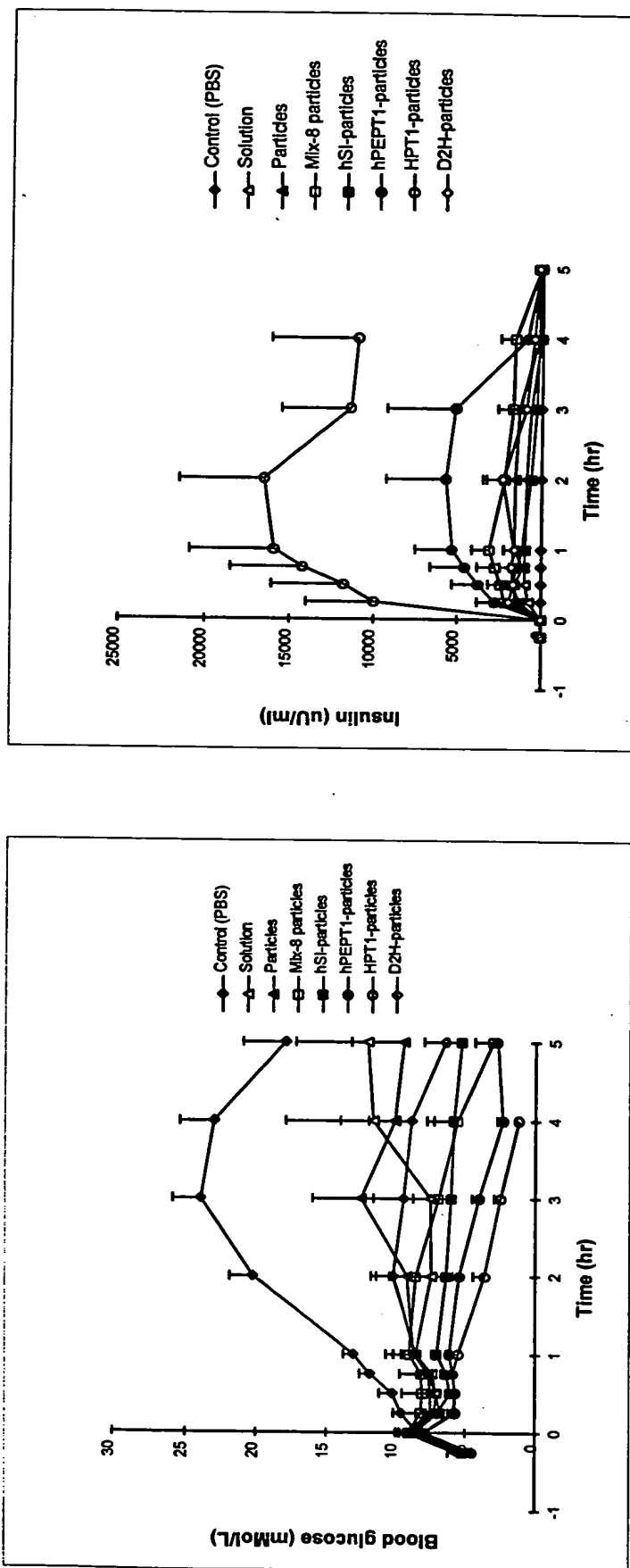


A



B

Fig. 17



A

B

Fig. 18

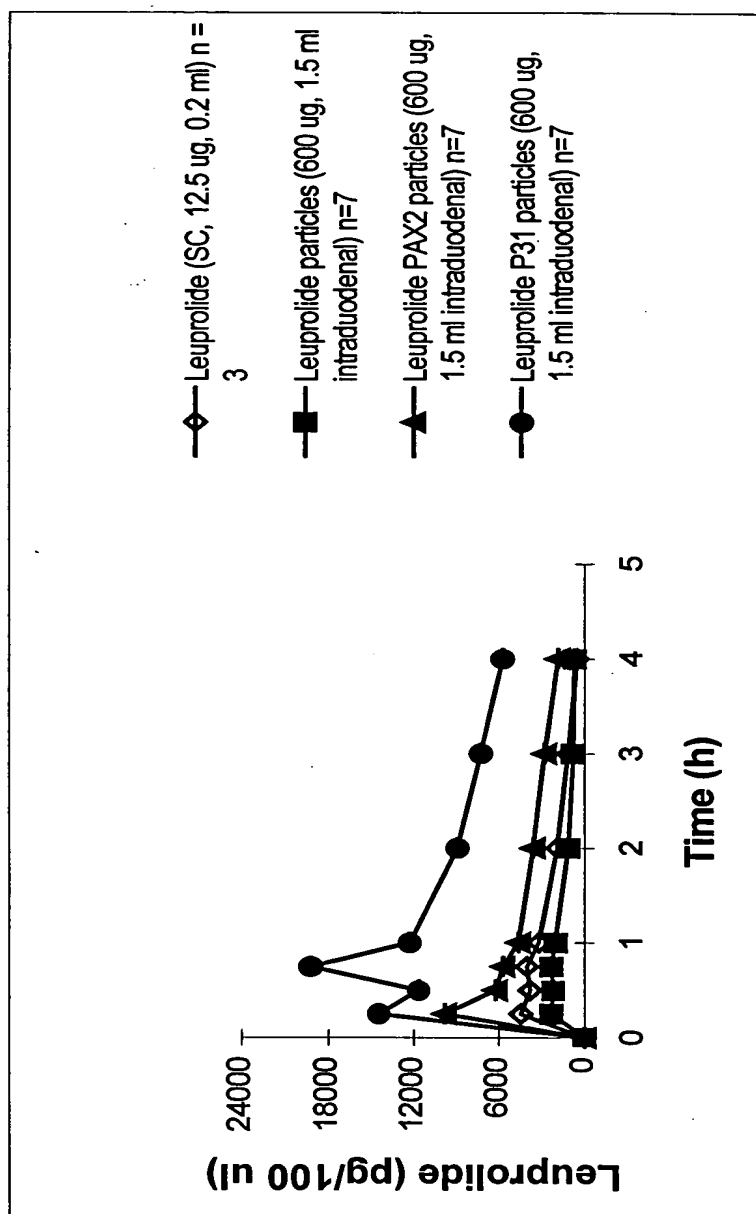


Fig. 19

P31 AA Seq. Position	Known Protein	Homologous Seq. Position
12-34	Fasciculin 2	10-32
4-12	Mesentericopeptidase	54-62
15-31		175-191
26-39	Core protein (Hepatitis C virus)	5-18
26-39		11-24
26-39		21-34
26-39		38-51
23-30		39-55
25-39		41-55
26-39		51-64
16-39	PT-NANBH Polyprotein N-terminus	51-64
28-40	AL2 protein (Caenorhabditiselegans)	70-82
26-38	Capsid protein (Hepatitis C virus Type 3g)	48-60
26-39	Genome polyprotein (Hepatitis C virus)	57-70

Fig. 20

DCX8AA Seq. Position	Known Protein	Homologous Seq. Position
20-27	Endo-1,4-Beta-D-Glucanase	78-85
30-37		221-228
21-34	P-Hydroxybenzoate Hydroxylase	285-298
5-15		54-64
7-21	Cytochrome	50-64
7-21	Cytochrome C3	50-64
	Trimethylarnine Dehydrogenase	208-219
32-43		396-407
30-37	Gag-JunD fusion protein	24-31
26-30		16-20
23-44	Secretin precursor, N- prosecretin, secretin ainide	18-39
33-44	T-cell receptor V beta chain	15-26
27-33		3-9
23-44	Secretin precursor pir	18-39
31-44	Hypothetical protein V (Synechocystis)	275-288
24-30		251-257
23-43	Putative RNA binding protein	230-250
28-40	Mu son of sevenless 1	1-13
24-35	Neuropeptide precursor	80-91
29-43		5-19
23-43	RNA-binding protein (Macacafascicularis)	230-250
23-43	RNA-binding protein (Homosapiens)	230-250
23-43	Autosomal gene – azoospermia factor	230-250
25-38	Collagen	25-28
24-35		4-15
29-41	Probable cell growth regulator	306-318
24-35	Ribosomal protein S2	24-35
T6-39		182-185
24-44	Caenorhabditis elegans	296-316
23-34	pid:e208155 (Homo sapiens)	61-72
36-43		116-123

Fig. 21A

DCX8A Seq. Position	Known Protein	Homologous Seq. Position
24-38	Xylulose Kinase	16-30
24-39	Caenorhabditis elegans	57-72
26-42		65-81
27-33	Hypothetical protein – phage BZ13	22-28
35-39		31-35
30-42	Cerebellin-like glycoprotein	2-14
8-22	DNA Primase	170-184
2-7		76-81
5-21	Coat Protein (Bean common mosaic virus)	12-28
5-21	Coat protein (Bean common mosaic virus)	33-49
5-21		19-35
5-21	Polyprotein (Bean common mosaic virus)	215-231
5-21		39-55
5-21	Nib protein/coat protein (Cowpea aphid-borne mosaic virus)	92-108
2-13	MHC class I Pipi (Pithecia)	111-122
14-22		326-334
3-19	Talin (Caenorhabditis elegans)	1538-1554
2-9	Acetamidase pir	359-366
9-20		483-494
10-16	Rhizobium etli strain	134-140
17-30		173-186
31-39		200-208
2-11	Neurotoxin 1 (toxin B) A. Stokesi	7-16
12-33		26-47
21-27	Suid herpes virus 1 early protein	425-432
30-43		51-64
13-42	Rice cDNA partial sequence	50-151
8-15	Fusion protein	24-31
4-8		16-20
1-22	Secretin precursor, N-prosecretin, secretin-amide	18-39
11-22	T-cell receptor V beta chain	15-26
5-11		3-9
9-22	Hypothetical protein	275–288
2-8		251-257

Fig. 21B

DCX8A Seq. Position	Known Protein	Homologous Seq. Position
1-21	Putative RNA binding protein	230-250
6-18	Hypothetical protein-mouse pir	1-13
2-13	Neuropeptide precursor	80-91
7-21	orf3-human	5-19
1-21	RNA-binding protein	230-250
13-16	Collagen	25-28
7-19	Probable cell growth or differentiation regulator	306-318
2-13	Ribosomal protein S2	14-25
14-17		182-185
2-22	Caenorhabditis elegans	296-316
1-12	Homo sapiens	61-72
14-21		116-123
2-16	Xylulose Kinase	16-30
8-15	T cell receptor delta chain	55-62
5-8		12-15
8-17	Seq. 43 from patent US	12-21

Fig. 21C

DAB10 AA Seq. Position	Known Protein	Homologous Seq. Position
13-34	1,3-Beta-Gllucanase	231-252
3-11	Photosynthetic Reaction Center	20-28
16-27		128-139
28-35	MYB Proto-Oncogene Protein	131-138
5-18		32-45
23-36	Lysozyme Mutant	130-143
28-35	Lipase	400-407
3-15		159-171
3-37	Trypsin	169-203
13-34	1,3-1,4-Beta-Glucanase	232-253
4-10	Lactate Dehydrogenase	190-196
11-7		244-250
4-10	Apo-Lactate Dehydrogenase	190-196
11-17		244-250
4-10	Lactate Dehydrogenase	191-197
11-17		245-251
16-26	Ovotransferrin	240-250
23-36	Genome Polyprotein Matrix Protein	1022-1035
14-20	Rous sarcoma virus	43-49
2-12		13-23
14-20	Hypothetical protein-avian leukosis virus	43-49
4-20	T cell receptor delta chain variable region	1-4
14-18		12-16
2-12	Gag Polyprotein-avian endogenous virus RAV-0	139-149
14-20		169-175
	p19 Protein-avian erythroblastosis virus	189-199
14-20		219-225
7-19	ALI protein-potato yellow mosaic virus	222-234
3-22	Endo-1,4-beta glucanase	186-205
6-18	I a protein-brome mosaic virus	430-442
2-12	Gag polyprotein-Fujinami sarcoma virus	186-196
14-22		216-222
2-12	Gag protein-Rous sarcoma virus	190-200
14-20		220-226
1-12	Corticotropin-like intermediate lobe peptide	7-18
1-22	Gene product (Caenorhabditis elegans)	4-25
31-37	T cell receptor delta chain	56-62
26-39		12-15
26-37	Lysozyme Mutant	133-144

Fig. 22

ATG	TCC	CCT	ATA	CTA	GGT	TAT	TGG	AAA	ATT	AAG	GGC	CTT	GTG	CAA	CCC	48
Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro	
1				5					10					15		
ACT	CGA	CTT	CTT	TTG	GAA	TAT	CTT	GAA	GAA	AAA	TAT	GAA	GAG	CAT	TTG	96
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	
			20					25					30			
TAT	GAG	CGC	GAT	GAA	GGT	GAT	AAA	TGG	CGA	AAC	AAA	AAG	TTT	GAA	TTG	144
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	
		35					40					45				
GGT	TTG	GAG	TTT	CCC	AAT	CTT	CCT	TAT	TAT	ATT	GAT	GGT	GAT	GTT	AAA	192
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	
	50					55					60					
TTA	ACA	CAG	TCT	ATG	GCC	ATC	ATA	CGT	TAT	ATA	GCT	GAC	AAG	CAC	AAC	240
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	
65					70					75					80	
ATG	TTG	GGT	GGT	TGT	CCA	AAA	GAG	CGT	GCA	GAG	ATT	TCA	ATG	CTT	GAA	288
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
				85				90						95		
GGA	GCG	GTT	TTG	GAT	ATT	AGA	TAC	GGT	GTT	TCG	AGA	ATT	GCA	TAT	AGT	336
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
			100					105					110			
AAA	GAC	TTT	GAA	ACT	CTC	AAA	GTT	GAT	TTT	CTT	AGC	AAG	CTA	CCT	GAA	384
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
		115					120					125				
ATG	CTG	AAA	ATG	TTC	GAA	GAT	CGT	TTA	TGT	CAT	AAA	ACA	TAT	TTA	AAT	432
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
	130					135					140					
GGT	GAT	CAT	GTA	ACC	CAT	CCT	GAC	TTC	ATG	TTG	TAT	GAC	GCT	CTT	GAT	480
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
	145				150					155				160		
GTT	GTT	TTA	TAC	ATG	GAC	CCA	ATG	TGC	CTG	GAT	GCG	TTC	CCA	AAA	TTA	528
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
				165				170						175		
GTT	TGT	TTT	AAA	AAA	CGT	ATT	GAA	GCT	ATC	CCA	CAA	ATT	GAT	AAG	TAC	576
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	
			180					185					190			
TTG	AAA	TCC	AGC	AAG	TAT	ATA	GCA	TGG	CCT	TTG	CAG	GGC	TGG	CAA	GCC	624
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
		195					200					205				
ACG	TTT	GGT	GGT	GGC	GAC	CAT	CCT	CCA	AAA	TCG	GAT	CTG	GTT	CCG	CGT	672
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	
	210					215					220					
GGA	TCC	CCA	GGA	ATT	CCC	GGG	TCG	ACT	CGA	GCG	GCC	GCA	TCG	TGA		717
Gly	Ser	Pro	Gly	Ile	Pro	Gly	Ser	Thr	Arg	Ala	Ala	Ala	Ser			
225					230					235						

Fig. 23